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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the term' score distribution.

SUMMARIES

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446.8	454	461.8	494 2	435 4	506 4	Score
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ALIGNMENTS

COMPAND CONTRACTOR OF THE CONT	JOURNAL MEDLINE	TITLE	REFERENCE	ORGANISM	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 AV600094/c LOCUS DEFINITION
Contact: Yoshikazu Sugimoto Animal Genetics Division Shirakawa Instituto of Anima! Conetics Odakuru, Nishiyo, Nishi Shirakawa, Fukushina 961 6061, Japan Tel. 81:248-25-5641 Fax: 81-248-25-5725 Bmail: kazusugi@cocoa.ocn.ne.jp Single pass sequencing.	poly(A) tail removed CDNA ilbraries and determination of 36,000 bovine ESTs Nucleic Acids Res. 29 (22), E108 (2001) 21570554	and Sugimoto, Y. Establishment of a high throughput (2) sequencing system using	Bovidae: Bovinae: Bos. 1 (bases 1 to 574) Takasaya A. Hirotsano S. Tokur. Titohasaya A. Sacakiana Asoln.	Bos taurus Dukaryeta, Metazea, Cherdata, Cramiata, Vertebrata, Euteleostomi; Mammalia: Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	EICA048A0Z 5', mRNA sequence. AV600094 AV600094.1 GI:9718839 EST. COW.	AV600094 574 bp mRNA linear EST 27-NOV-2001 AV600094 Bos taurus cartilage fetus Bos taurus cDNA clone

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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAURNAL
                                                                                                                                                                                                                                                                                                                                 1688 ACTICCCCTCCCTCCATAAGGCAGTTCTATTTCCAGTTTTTTAAGGAATCTCCACACT 1747
                                                                                                      2107 - 361 F. ISANGGETG F. GITTE GOTT FOR TANDALIST SET (SANGALLITIA) 2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1808 FCTCCACACCCCCCCCCAGCATTTATTATTTCTAGACTTTTTGGATCGCAGCCAATCTGACT 1867
                                         2167 ACCTTAATTAGGTCCCATTTGTTTATTTTTGCTTTTATTTTGCAAT 2211
                                                                                                                                                                      187
                                                                                                                                                                                                                                                  247
                                                                                                                                                                                                                                                                                                                                                                                                                                                               8381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.27 TCTCCACACCACCAGCATTIATIATITSTAGACTTITGGGTCGCAGCCATTCTGACT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547 AĞTĞĞĞATTĞCTĞĞATÇATAAĞĞÇAĞTTETATFFCCAĞTFFFTTTAAĞĞAAFCFCCAÇACIF 488
    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                AGATCTTTGGCCGAITH HOATINGGCATHAITH ECTGGAGTIGAGCTGAAGAGAAGACT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGTGAAATGGTACCTCATAGTGG-TTTGATTTTGCTCTGATAATGAGTGATGTT 1926
HELLING TOCCATTIGET HALF STEED TO TAIT TOCAAT
                                                                                                                                                                      TGCTTGTATATTTTTGAGATTAGTTGTTTTGTCGGTTGCCTCATTTGTTGTCCC
                                                                                                                                                                                     RCCTTGTATATTTTTTGAGATTAGTTGTTGTCGCTTGCTTCATTTTGCTATATTTTTCTCC 2106
                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGTGAAATGATATCTCATAGTGGTTTTGATTTGCATTFCTCTGATAATGAGTGATGTT
                                                                                   CATTCTGAAGGCTGTCTTTTCACTTTTGCTAATAGTTTCCTTTTGATGTGCAGAAGCTTTTA 68
                                                                                                                                                                                                                                                                                            ACTICITIFGGCCCAFFFFFTGAFFGGGTCCFFFAFFFFFTCFGGAGTTGAGCTGTAGCAGT 2046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shiranawa Institute of Animai benetics
Odakura, Nishigo, Nishi shirakawa, Fukushima 961–8061, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 547)
Takasuga, A., Hirotsunc, S., Ttob. R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asimal Genetics Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact. Koshikasu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              poly(A) tail-removed cDNA libraries and determination of 46,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Establishment of a high throughput EST sequencing system using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Sugimoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single pass sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 29 (22), E108 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone was obtained from a polyA-deleted cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was deleted from a Not1 site_1: Sal1; Site_2: Not1; Foly A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="brain"
/dev_stage "fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib-"Bos taurus brain fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xre1="taxon:9913"
/clone="EIBR050C05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.3%;
97.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 495.4; DB 10; Length 547; Pred. No. 1.5e~78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jitokrete.A., Sazaki, B., Aso, H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                         1826 CATTATTATTTGTAGACTTTTGGATCGCAGCCAATCTGACTGGTGTGAAATGGTACCTC 1885
                                                                                                                                                                                                                                                                                                                                                                                                                                      1526 TAATACTCCATTGTGTATATGTACCACAGCTTTCTTATCCATTCATCTGCTGATCGACCAT 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1466 GGCTCCAGTTTCATCCACCTCATTAGAACTGATTCAAATGTATTCTTTTTAATGGCTGAG 1525
                                                                                                                                                                                                                                                               199
                                                                                                                                                                                                                                                                                                                                                                        1586 - СТАККТТКО ТТООАТКТОСТВВОТАТТА1 АААОАӨТӨСТӨГӨӨТӨЛӨӨТӨӨТТӨӨКӨТАСАС - 154 5
                                                                                                                                                                                                                                                                                                                             139 CTAGGTTGCATGTCCFGGCTATTATAAACAGTGCTGCGATGAACATTGGGGTACAC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 GTCCGCAGTTTCATCCACATTATTAGAACTGATTCAAATGCATTCTTTTTAATGGCTGAG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loca
                                                                                                                                                                                                                                        GREATOTOTTTCAATTOTEGETTT-OTOGGTGTGTGTATGCCCAGCAGTGGGATTGCTGGGTCA 257
                                                                                                                                                                                               TAAGGCAGFFCFAFFFFCCAGFFTTTTTAAGGAATCFCCACACFGFTCTCCATAGFGGCFGT 1765
                                                                                                                                                                                                                                                                                                                                                                                                               TAATACTCCATTGTGTATATGTACCACTGCTTTCTTATCCATTCATCTGCTGATGGACAT 138
                                                                    ACTAGTTTGCATTCCCACCAACAGTGTAAGAGGGTTCCCTTTTCTCCACACATCCTCTCCAG
                                                                                                        ACTAGITIGGATICCCA/CAACAGIGIAAGAGGTICCCTTTTCCCACACCCTCTCCAG 1825
                                                                                                                                                      TAIGGCAGITITATITCCAGITITITAAGGAAICTCCACACIGITCTCCATAGIGGTGGCTGT 317
AV595123 Hos taurus cartilage fetus Bus taurus cDNA elone
PICA017g01 5', mkNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CO¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV595123.1 GI:9711673
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single pass sequencing. This clone was obtained from a polya deleted {\tt CDNA} library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bovine ESTs
Nucleic Acids Res 29 (22), E108 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Sugimoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: kazusugi@cocoa.ocn.ne.jp
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Tel: 81-248-25-5641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Establishment of a high throughput EST sequencing system using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takasuqa,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Kuthetia, Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fukanyofa; Motaroa; Oʻerdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Kuthetia, Cetartiodaetjia, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tail-removed cDNA libraries and determination of 36,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Cryanian "Bos Caurus"
/db_xref="taxon:9913"
/rlone="F16A017601"
                                                                                                                                                                             /dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Hos taurus cartilage fetus"
/tissue_type="cartilage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 30; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 494.2; DB 10;
Pred. No. 2.3e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 598;
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                                                                                                                                             ORIGIN
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                                                                                                                                                                BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
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                                                  Matches
                                                                        Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
1333 TGTTCTATACATGAGTGTCTC1 FFFGCTG1616GGTACACCGGG TATTGTTACCATCTTT 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1942 TGTTTGTTAGCCATCTGTATGTCIIIIII.ovAvAAAAIGTCTAIIIAGIICIIIIoveCCAI 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   498 TGTTTGTTAGCCATCTGNATGTCTTCTTTTCCAGAAATGTCTGTTTAGTTCTT11GGCCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 CATTIATIGITIGIAGACITIGGGATAGCAGICATICIGACIGGIGIGAAAIGGTACCTC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE653999 489 bp mRNA linear 278903 MARC JBOV Bos taurus cDNA 5', mRNA sequence BE653999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence evaluation of four pooled tissue normalized boying cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith, J.F.L., Grosse, W.M., Freking, B.A., kelberts, A.J., Stone, R.T., Gasas E. Wray T.F. Whire T. Cho, J., Fahrenkrug, S.C., Bennert G.G.L. Heaton, M.P., Laegreid, W.W., Rohrer G.A., Chitko-McKown, C.G., Fercea, G., Böll, J., Karamycheva, S., Liáng, F., Quackenbush, J. and
                                             h 15.1%; Score 461.8; DB 12; Similarity 96.5%; Pred. No. 1.5e-72; 0: Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: 70 row: J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e., Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebiata, Euteleostomi;
Mammalla, Eutheria, Cetaitlodaet<sub>i</sub>la, Ruminantia, Fessia, Bossidea
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                                                                                                                                                                D
                                                                                                                                                       /note-"Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall; Library made irom pooled tissue irom marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and tetal longissimus muscle."

a 111 c 93 g 187 t
                                                                                                                                                                                                                                                                          /tissue_type="pooled"
/lab_host="DH10H"
                                                                                                                                                                                                                                                                                                                          /clone_lib-"MARC 3BOV"
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                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus"
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410 Agri/Por, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
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The sequence best matches gb:BTU15731 (Bos taurus samatobropic
receptor gene, exon 1 and liver-specific promoter region)in main
database at high score of 847.0 and E value of 0.0
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                          780 492 4265
/clone lib="Hovine Mixed Adipose cDNA library"
/sex="two males and one female mixed"
                                                                                                           Location/Qualifiers
                                             /db_xret-"laxon:9913"
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Contact: Yoshikazu Sugimoto
                         bovine ESTs
Nucleic Acids Res. 29 (22), E188 (2001)
                                                                      Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,00
                                                                                                           and Sugimoto, Y
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodaetyla; Ruminantia; Pecora; Bovoidea;
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/lab_host="XLI-BlueMRF'strain"
/hote="Grgan: Subsutaneous, Omedial, Mesenteric adipose;
Vector: Uni-2%AFXK; Site_1: EcoKI: Site_2: Xho I"
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/cell_type-"Adipocyte"
                                                                                                                           . Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H
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96.7%;
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Pred. No. 3.6e-71;
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Animal Genetics Division

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                                                                                                          KEYWORDS
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                                                                                                                                                                ACCESSION
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                                                                                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                            AW669746
                                                        ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                       2201 TTATTTCCAATATTCTGGGAGGTGGGTC 2228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1962 GTCTFTTTGGAGAAATGTCTATTTAGTTCTTTGGCCCATTTTTTGATTTGGTCGTTTAT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1902 CATTTCTCTGATAATGAGTGATGTTTGAGCATCTTTTCATGTGTTTTGTTAGCCATCTGTAT 1961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1843 CTTTTGGATCGCAGCCAATCTGACTGGTGTGAAATGGTACCTCATAGTGG-TTTGATTTG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1783 CCAACAGTGTAAGAGGGTTGCCTTTTCTCCACACCCCTCTCCAGCATTTATTATTTTGTAGA 1842
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                                                                                                                                                                                                                                                                                                                                                    492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 GTCTTCTTTGGAGAAATGTCTATTTAGGTCTTTGGCCCATTTTTTTGATTGGGTCGTTTAT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 CTTTTGGATCGCAGCCATTCTGACTGGCATGAAATGGTACC.CATTGTGGTTTTGAITTG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 CAGTTTTTTAAGGAATGTCCACACTGTTCTCCATAGTGGCTGTACTAGTTTGCATTCCCA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 CCAACAGTGTAAGAGGGTTCCCTTTTCTCCACACCGTCTCCAGCATTTATTGCTTGTAGA 131 ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                 TTATTTCCAATATTCTGGGAGGNGGGTC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCCTTTGTTGTGCAGAAGCTTTTAATTTTAATTTAAGGTCCCATTTGNTTATTTTTGCTT 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone was obtained
                                                     Bos taurus
                                                                                                          AW669746.1 GI:7526260
EST.
                                                                                                                                                                              AW669746 483 bp mRNA linear 113279 MARC 1HOV Hos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: kazusugi@cocca.ocn.ne.jp
Rukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Cetarticdactyla, Ruminantia, Pecura, Bovoidea
                                                                                                                                                                AW669745
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/note-"Vector: pZL1; Site_1: Sal1; Site_2: Not1; Foly A
/was deleted from a Not1 site"
/ 127 : "52 y 275 t 19 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="E11,0039G09"
/clone_lib="Bos taurus lung fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Bos taurus"
/db_xret-"taxon:9913"
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1. .707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1519 GGCTGAGTAATACTCCATTGTGTATATGTACCACAGCTTTCTTATCCATTCATCTGCTGA 1578
                       1938 CATGTGTTTGTTAGCCATCTGTATGTCTTTTT 1969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1579 TGGACATCTAGGTTGCTTCCATGTCCTGGCTATTATAAACAGTGCTGCGATGAACATTGG 1638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GGTACACGTGTCTCTTCCCCTTCTGGTTTCCTCAGTGTGTATGCCCCAGCAGTGGGATTGC
                                                                                                                                                                                                                                                                         241
                                                                      361 GTACCTCACAGTGGTTTGGATTTGCATTTCTGTGATAATGAGTGATGTTCAGCATCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGCTGAGTAATACTCCATTGTGTATATGTACCACAGCTTTCTTATCCATTCATCTGCTGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGACATCTAGGTTGCTTCCATGTCCTGGCTATTATAAACAGTGCTGCGATGAACATTGG
                                                                                                  GTACCTCATAGIGGTTT-GATTIGCAIFICICTGATAATGAGTGATGTTGAGCAICTTTT 1937
                                                                                                                                                            TOTOCASCATTATTATTTGTASACTTTGSATGCASCCATTCTSACTSSISISAAA15
                                                                                                                                                                                                                                                                 TGGCTGTACTAGTTTGCATTGCCACCAACAGTGTAAGAGGGTHCCCFTFFCTCCACACCC
                                                                                                                                                                                                                     TCTCCAGCATITATTATTTGTAGACTTTTGGATCGCAGCCAATCTGACTGGTGTGAAATG 1878
                                                                                                                                                                                                                                                                                                                                                                    TGGATCATAAGGCAGTTCTATTTCCAGTTTTTTAAGGAATCTCCACACTGTTCTCCATAG
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Smith, T.P. L., Grosse, W.M., Freking, E.A., Beberts, A.J., Stone, R.T., Smith, T.P. L., Grosse, W.M., Freking, E.A., Beberts, A.J., Stone, R.T., Casas, E., Mray, J.E., White, J., Cho, J., Fanrenkrug, S.C., Beisett, G.L., Healon, M.P., Laegreid, W.W., Röhrer, G.A., Chitko-McKown, C.G., Fertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Sequence evaluation of four pooled tissue normalized bovine cDNA libraries and construction of a gene index for cattle genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fiate, 168 row, r column, 8 Seq primer: AFTTAGGTGACACTATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 402 762 4366
Fax: 402 762 4390
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PO Box 166, Clay Center, NE 68933-0166, USA
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Similarity 98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Smith TPL
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Library made from pocled tissue from lymph node, ovary,
fat, hypothalamus, and pitutary."
10/c 99 q 177 t
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/tissue_type="pooled"
/lab_host="DH10H"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Overy Match 15.0%; Score 4:0.8; DB 10; Length 447; Best Local Similarity 99.3%; Pred. No. 5e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE
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                       1896 GAPPTOCAPTTCTCTCTGATAATGAGTGATGTTGAGCATCTTTTCATGTTTTCTTTAGCCAT 1955
                                                                                                                                                                                                 //// FIGUSTACCAACAACAACAACAACAACACCITTICICCACAACACCCICTACAACAALIAALIAILI 1836
                                                                                                                                                                                                                                                                                                                                1717 TATETICCAGEFFETERAAGGAATCFCCACAGAGTECECCATAGTEGC/EGFACTAGFFFECCA 1776
                                                                                                                                                                                                                                                                                                                                                                                                                                1.657 COPPORGETTOCICACTICICATICICATICACICAGCAGCAGTICGGGGTTGCTGGATICATIAAGGCAGTITC 17.16
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                                                                                                                       TH37 TGTACACTTTTTGGATCGCAGCCAATCTGACTGGTGTGAAATGGTACCTCATAGTGG-TTT 1895
                                                                       267 TGTASACHITISGATGGAAGGAAGGAATGAGTGAAATGTAAATGGTAACCTCATAGTGGTTTT 208
                                                                                                                                                                                                                                                                                                                                                                              447 CCTTCTGGLFECCICAGEGETALGGCCAGCAGEGGALGGCEGALGALAAGGCAGTEC 388
                                                                                                                                                                                                                                                                                   387 FATTICCAGEFFFFTAAGGAATCTCCACACTGTTCTCCATAGTGGCTGTACTAGTTTCCA 328
                                                                                                                                                                               TECCCACCACCACAGEGEAAGAGGGEECCCEETTECECCACACCCECECCCAGCAFFTEATTAFF 268
                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith*email.marc.usda.gov
Single pass sequencing. Hases called and trimmed with phred
v0.980994.c. Vector [dentified by *ross_match with the rice
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
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Smith, T P L , Grossi
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Plate: 27 row: P column: 2:
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Mammalia; Eutheria; Cetartiodaetyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                smith T.P.L. Grosse W.M. Freking B.A. Poberis, A.D. Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrud, S.C., Hemett, G.I., Heaton, M.P., Laegreid, W.W., Kohrer, G.A., Chirko M.Kown, C.G., Pertaa, G., H.Lt., L. Kararycheva, S., Diang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
Single pass sequencing. Hases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the _minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
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                                                                                                          /note-"Vector: pCMV SPORT6: Site_1: Not1: Site_2: Sal1: Library made from pooled tissue from day 20 and day 40 embryos."
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                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center
PO Hox 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
Plate: 66 row: D column: 24
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                       Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence evaluation of four pooled rissue normalized bowine eDNA
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                                                                                                                                                                                                PCR PRimers
                                                                                                                                                                                                                    and -minmatch 12 options.
                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                   21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                         libraries and construction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keele, J.W.
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                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 54)
                                                                                   Location/Qualifiers
  /clone_lib="MARC 4BOV"
                        /db_xre1-"taxon:9913"
                                        /organism-"Bos taurus"
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                                                                      . 54 1
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                                           MEDITINE
                                                                 JOURNAL.
                                                                                                          TITLE
                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1743 ACACTGRERCECTATAGRGGCTGTACTAGTTTGCATTCCCACCAACAAACGTAAGAGGGTTC 1802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2221 COMCCOMO 2228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGACTGGCGTGAAATGGTACCTCATTGTGGGTTTTGATTTGCATTTCTGATAACAAGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTCCCATTCTGAAGGCTGTCTTTTCACCTTACTAATAGTTTCCTTTAATGTGCAAGAG 2160
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             21180013
Contact: Smith TPL
                                                          Sequence evaluation of four pooled tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                            Smith, T.P.L., Grosse, W.M., Freking, H.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fairenkrug, S.C., Bennett Gasas, E., Laegreid, W.M., Robrer, G.A., Chitko-McKown, C.G., Periea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                   BI680692.1 GI:15633606
EST.
USDA, ARS, US Meat Animal Research Center
                                                                                                                                 Keele, J.W.
                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora, Bovoidea;
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Similarity 94.3%;
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/lab_bost="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1507 G.TALIATAAAAA IGCIGGATGAACAAT GGGTACAACGTCTCTTTCCCTLCTGGTT 1666
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                                                                                                UNL-P-FN c) 1:03 0:UNL.S1 UNL-P-FN Sus scrota cDNA clone UNL-P-FN c)-1:03-0:UNL 3', mRNA sequence
BI184173.1 CT:14658582
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Plate: 127 row: F column:
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74 c 123 q 115 t
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/lab_bost="DH10H"
/mete="Vector: pCMV speace site_1: Wat!, site_2 sgl!,
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/obc_vret="layon-gala"
/olone_lib-"MARC [BOV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1762 CTGTACTAGTTTGCATTCCCACCAACAGTGTAAGAGGTTTCCCTTTTCTCCACACACCCTGT 182
                                                                                                               1702 ATCATANGCIASTICTATTICCAGITITITAAGGAATCICCACAGIGITCICCATAGIGG 1760
                                                                                                                                                                                                   1642 Adaminicicililacciicimalificticanigiginalocca.Andminnatticteg 1701
                                                                                                                                                                                                                                                                                                                                                 1582 ACATCTAGGTTGCCTGCCATGTCCTGCCTATTATAAACAGTGCTGCGATGAACATTGGGGT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                      228 ALCAMISSIASILCIAISIIIASIIIICIGAGAAICICCAIACIGCCACAGTGG
                                                                                                                                                                        168 TCATIGTGTGTGTGCGAGINGTGGTTTTCTCTGTGGATAGATGCCCAGGAGTGGGGATTGCTGG 227
                                                                                                                                                                                                                                                                                     108 ACATTAGGITGTITCCALGITITGGGCIGITGIMALAGIGCIGCAGIAAACALIGGAGT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          48 TGAGTAATATTCCAITGIGLALAIGIACCACACTCTTGAICGACTCCTCTGITGAIGG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Animal Science
University of Nobraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 492 472 6352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLYA-Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand with and therefore this may represent a benafide pary A tail. The sequence tay present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caetano,A.R., Johnson,R.K. and Pomp,D. Generation and Sequence characterization of a normalized cDNA library from swine ovarian follicles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 745)
Caetano, A.R., Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  normalized porcine ovarian follicles library
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Mammalia; Eutheria; Cetartiodaetyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host-"PHIOB (Life Technologies)"
/note-"Vector: p1773D-bac (Pharmacia) with a modified
/note-"Vector: p1773D-bac (Pharmacia) with a modified
polylinker; Site; not 1; Site;2; Eco RJ, The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a string of 5-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the library UNL-P-F2. The tag is a string of 5-6 mucleofides present between the Not 1 site and the oligo dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAG_TISSUE=porcine ovarian tollicles
TAG_SEO-CACACT*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS
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Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 2703)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duke University Medical Center
Box 2610, MSRB, Room 117, Durham, NC 27710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Bepler G
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                                                                 13.9%;
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SOURCE

ORGANISM

EST. COW. Bos taurus

Bovidae; Bovinae; Bos.

Eukaryola; Metazca, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea BE074298
LOCIS
DEFINITION
ACCESSION
VERSION
KEYWORDS

BF074298.1 GI:10867809

BF074298

BE074298 569 bp mRNA linear 221675 MARC 2BOV Bos taurus cDNA 57, mRNA sequence.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fixith, T.P.L., Stusse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence evaluation of four pooled-tipsue normalized bovine cDNA libraries and construction of a gene lindex for cattle
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Plate: 80 row: C column: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 402 762 4366
Fax: 402 762 4390
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/lab_host="DH10B"
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Matches 587;
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                                                1509 TOTTTTAATGAGTAATAGTGAATAGTGAATGAAGGTAAGAGGTAAGTAATCCATT 1568
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This clone has the following problem: incomplete processing.
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CDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIH MGC Project Ush. http://mar.nci.nih.gav
Contact: MGC help desk
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Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hy>- h-a-to---hy/ohay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapieus
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/clone_lib="NIH_MGC_87"
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                                                             1755 TOFTGAGTTTAAFTAGATCCCATTTGTCAAFTTTGGCTTTTTGTTGCCATTGCTTTTGGTG
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                                                                                                                                                                                                                                                                                1982 TATTIAGTICTTIGGCCCATTTTITGATIGGGCGGTTATTTITGTGGGAGTIGAGCIGTA 2041
                                                                                                                                                                                                                                                                                                                                                                   1922
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                                                                                                                                                              2102 TCTCCCATTCTGAAGGCTGTCTTTTCACCTTGCTAATAGTTTCCTTTTGATGTGCAGAAGC 2161
                                                                                                                                                                                                                               2042 GGAGTTGCTTGTATATTTTTGAGATTAGTTGTTTGTCGGTTGCTTCATTTGCTAFTATTT 2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2291 TAAACATAIGTGTGCATGTGTTTTTATAGCAGCATCATTTATAATCCTTTGGGTATATAC 2232
                                                                                              TTTTAAGGTTAATTAGGTCCCATITGTTTATTTTIGCTITTATTTCCAMIATICIGGGAG 2221
                                                                                                                             TOTOCOCATTOTOTAGOTTCCCTGTTCACTCTGATGGTGGTGCTTTTTTTGCTGTGCAGAAGC
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